(Bayesian) regression models

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Contents

- 1. Linear regression models (LM)
- 2. Linear mixed effects models (LMM)
- 3. Bayesian linear mixed effects models (BLMM)

Simulated data

- ▶ Normal distributed data for two conditions *a* and *b*
 - ► *simDataContinuous*.*R*: Continuous predictor
 - ► *simData.R*: Discrete predictor
 - ► simDataSubjRE: Discrete predictor and by-subject variance added
- ▶ Population parameters are known!
- \rightarrow The underlying effect: β =50
 - ▶ I.e. difference between condition *a* and *b*
 - Lets try to uncover this effect ...
 - Open file AntwerpWS2017.Rproj

- ► Single level regression model; ordinary least squares (OLS)
- ▶ Linear change in the data given a predictor variable
- ▶ Predictor can be continuous (e.g. frequency: 0 100) or discrete (e.g. frequency: high vs. low)
- ► Allows multiple predictors

$$y_i = \alpha + \beta \times x_i + \epsilon_i \tag{1}$$

y: data

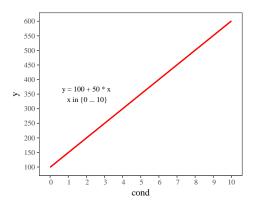
x: predictorx intercept

β: slope (gradient)

ightharpoonup ϵ : residual error (i.e. noise)

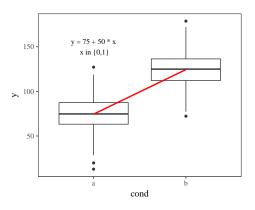
$$\epsilon_i \sim N(0, \sigma^2)$$
 (2)

- ► *R* function *lm*() (part of the base *R* package)
- ▶ Syntax: lm(outcome variable ~ predictor, data frame)
- ► Your turn: see *R* script *exercise_lm.R*



> head(data) cond y 9 465.8291 0 108.5086 9 569.3380 7 431.7700 7 449.9238 3 233.3673

Predictor *x* is continuous



Predictor *x* is discrete

> head(data) cond y b 105.10129 a 82.73471 b 104.00330 b 97.21434 b 101.53576 a 68.83296

See script *LM_model_discrete.R*

Population means are 75 for *cond a* and 125 for *cond b*.

- > m <- lm(y ~ cond, data)</pre>
- > summary(m)\$coef

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	74.499	0.804	92.626	< 0.001
condb	49.943	1.120	44.605	< 0.001

- (Intercept): y-value for cond = 0; here condition a
- ▶ condb: change from condition *a* (i.e. intercept) to *b*
- ▶ condition b + intercept is $t \times Std$. *Error* away from intercept
- ▶ Is that what we want?

► Treatment contrast (default): change from intercept

```
> contrasts(data$cond)
  b
a 0
b 1
  ▶ Sum contrast (effect magnitude): difference between a and b
> contrasts(data$cond) <- c(-.5, .5)</pre>
> colnames(contrasts(data$cond)) <- c("b-a")</pre>
> contrasts(data$cond)
   b-a
a - 0.5
b 0.5
```

Table: Treatment contrast

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	74.499	0.804	92.626	< 0.001
condb	49.943	1.120	44.605	< 0.001

Table: Sum contrast

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	99.470	0.560	177.678	< 0.001
condb-a	49.943	1.120	44.605	< 0.001

- Estimation of effect magnitude
- ▶ Linear function can account for and predict unobserved data
- Can account for additional sources of variance and potentially confounding variable by adding those to the model (co-variates)
- However, data are more complex than that:
 E.g. multiple observation per participant/item
- ► Solution: Linear mixed effects models

- Extension of linear regression
- ► Take into account within and between groups variance
- "Mixed": Fixed + random factors
- ► Fixed: systematic effect
- Random: non-systematic sources of variance; e.g. some participants are faster than others
- ▶ *lmer*(); part of *lme*4 (Bates, Mächler, Bolker, & Walker, 2015)

- New simulated data frame.
- ▶ Uncover known parameter $\beta = 50$
- Added by-subjects variance:By-subjects intercepts and slopes.
- ► Models *LM_observations_in_subj.R*
- ▶ What do you observe?
- ► What's the evidence that this parameter is different from 0 (i.e. null hypothesis)?

а

70.29821

```
> m1 <- lm(y ~ cond, data)
> m2 <- lm(ysubjmeans ~ cond, data.subj)
> m3a <- lmer(y ~ cond + (1|subj), data)
> m3b <- lmer(y ~ cond + (1+cond|subj), data</pre>
```

Table: Estimates (see *models_random_effects.R*)

	Estimate	Std. Error	t value	$\Pr(> t)$
m1	51.189	1.169	43.784	< 0.001
m2	51.189	2.823	18.135	< 0.001
m3a	51.189	0.860	59.506	
m3b	51.189	1.506	33.989	

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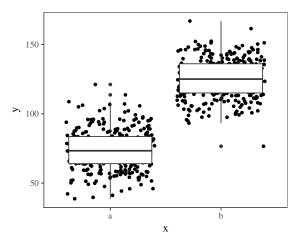
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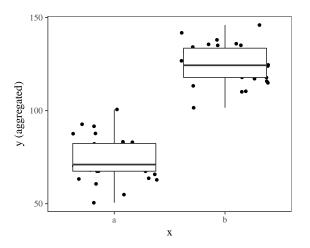
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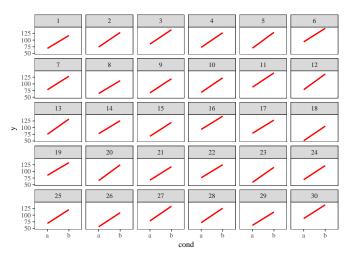
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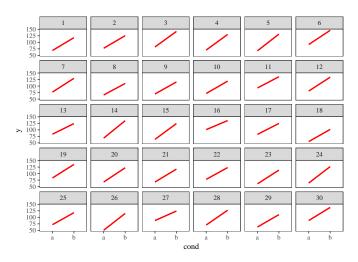
Simulated data



Simulated data, aggregated by subject and condition



Varying intercepts per subject: (1|subj)



Varying intercepts and slopes per subject: (1 + cond|subj)

- ▶ What about *p*?
- Unclear how to determine df (see Baayen, 2008)
- Alternatives:
 - ▶ t-value = 2 as lower bound for p < 0.05
 - Satterthwaite approximation *lmerTest* package
 - Model comparison using log likelihood ratio anova()
- ► See *LMER_pvalues*.*R*

- ▶ *p*-values do **not** tell us whether the difference is large enough to reject the null.
- ▶ This relies on the variance within each condition.
- ▶ We may reject the null for estimates that are too small to be sensible (e.g. $\sim 5ms$) if the variance is small enough
- ...or fail to reject the null for sensible estimates that if the variance is too large.
- ▶ It's not about a single value but a range.
- ▶ Is 0 a possible value?

- ▶ 95% confidence intervals (CI): If we were to repeat our experiment an infinite number of times and calculate a confidence interval each time, 95% of these intervals would contain the true parameter value.
- ► See simulation: http://rpsychologist.com/d3/CI/
- In other words, the estimate is merely the centre of a range of a imaginary range of other intervals which contains the population parameter.
- ▶ 5% of these unobserved ranges do not contain the true value.
- ► See exercises script *LMER*95%*CIs.R*

Advantages:

- Flexible models that account for the complexity of data
- ▶ Nested data: children nested in classes nested in schools
- Random effects: subject speed varies; effect varies across individuals; slopes and intercepts are correlated
- ► For a short but thorough intro see Vasishth and Nicenboim (2016)

Problem:

- Maximal random effects structure (Barr, Levy, Scheepers, & Tily, 2013):
 - (1 + cond|subject) + (1 + cond|item)
- Random effects can be added:
- i. (1 + cond|subject) accounts for varying conditional differences across subjects; not plausible in a between subjects design
- ii. (1 + cond|items) accounts for varying conditional differences across items; effect is stronger in some items
 Not plausible when there were no matched items

Problem:

- ► Maximal random effects structure (Barr et al., 2013): (1 + cond|subject) + (1 + cond|item)
- Convergence failure: over-parametrisation (Bates, Kliegl, Vasishth, & Baayen, 2015):
 - I.e. model is too complex for the data.
- ► Solution (i): remove random slopes until model converges
- ► Solution (ii): Bayesian Linear Mixed Effects Models

- ► Easier model fit: complex models converge by definition
- ► Answer the question we care about: what's the support for the hypothesis given the data?
- ► Intuitive interpretation: frequentist estimates are often interpret in a Bayesian manner (Nicenboim & Vasishth, 2016)
- ► Support for the hypothesis is not quantified by the implausibility of the null.

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Is p the probability that the null is true? What are we doing with p = 0.06?



- Bayesian inference based on the **Posterior** distribution approximated from the product of the **Likelihood** and the **Prior**:
 - (a) Plausible values for model parameters Prior.
 - (b) Probability model of the data generating process Likelihood.
- Sophisticated sampling techniques: Monte Carlo Markov Chain
- Sampling is used to approximate the posterior distribution by creating probability distributions of plausible parameter values.

Table: Interpretation of evidence

	NHST*	Bayes
Support for H_1	$P(data H_0)$	$P(H_1 data)$
Inference true effect	95% CI	CrI; HPDI

^{*}Null Hypothesis Significance Testing

Table: Interpretation of evidence

	NHST*	Bayes
Support for H_1	$P(data H_0)$	$P(H_1 data)$
Inference true effect	95% CI	CrI; HPDI

- ▶ Evidence in favour of H_1 :
 - NHST: indirect inference about H₁ based on the (im)plausibility of the data if H₀ were true.
 - ▶ Bayes: direct support for H_1 given the data.

^{*}Null Hypothesis Significance Testing

Table: Interpretation of evidence

	NHST*	Bayes
Support for H_1	$P(data H_0)$	$P(H_1 data)$
Inference true effect	95% CI	CrI; HPDI

- ▶ Intervals containing the true parameter value:
 - ▶ NHST: if we were to replicated a experiment a large number of times and calculate a CI each time, 95% of these intervals would include the true parameter value
 - ▶ Bayes: probability distribution of possible values for true parameter (e.g. 95% range)

^{*}Null Hypothesis Significance Testing

- Probabilistic sampling using Stan Hamiltonian Monte Carlo
- ► *R-*Stan interface (Stan Development Team, 2015)
- ▶ *R* packages for Bayesian LMMs: *rstanarm* (Gabry & Goodrich, 2016); *brms* (Bürkner, 2017); *rethinking* (McElreath, 2016)

See script BLMM.R: run the model now

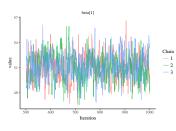
```
m <- stan_lmer(y ~ cond + (1 + cond | subj)
, prior_intercept = student_t(df = 1, location = 0)
, prior = student_t(df = 1, location = 0)
, data = data
, chains = 3
, iter = 1000
, cores = 4
, seed = 17)</pre>
```

- prior_intercept
- ▶ prior_slope
- ► chains
- ▶ iter
- cores
- seed

- student_t distributions have a location parameter and df: see script student-t-distribution.R
- Weakly informative priors: student_t(df=1)
- Other priors: normal(), cauchy(); also on other parameters (e.g. variance-covariance matrix)
- ▶ At least 3 chains to determine convergence.
- If model doesn't converge, increase iterations.

- Ensuring convergence;
 i.e. model has successfully determined a posterior.
- Compare data to posterior predictive values.
- ► Traceplots; hairy caterpillars
- ▶ \hat{R} = 1; Rubin-Gelman statistic (Gelman & Rubin, 1992)
- ► Example and exercises: *BLMM_modelchecks.R*

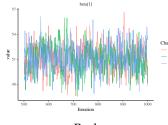
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Real

Traceplots

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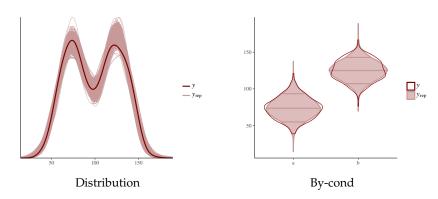


Real



Fake

Traceplots



Comparison of data and posterior predictive values

- ▶ Does the interval contain 0? Is 0 a possible parameter value?
- 95% credible interval (CrI): range of possible parameter values with equal probability mass assigned to each tail (percentile intervals)
- 95% highest posterior density interval (HPDI): interval that embraces the assigned probability mass; identical to CrI for symmetrically distributed posteriors
- ► Go through script *BLMM_CrI.R*

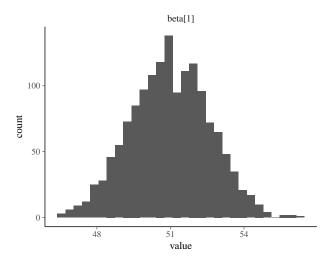
- ▶ Does the interval contain 0? Is 0 a possible parameter value?
- ▶ What's the probability that this isn't probable?
- ► $P(\hat{\beta} < 0)$: proportion of posterior samples that is smaller than 0 \rightarrow probability that parameter is smaller than 0 (i.e. speed-up)
- ► Go through script *BLMM_postprob*.*R*

- ▶ Does the interval contain 0? Is 0 a possible parameter value?
- ▶ What's probability of a slow-down/speed-up?
- ► $P(\hat{\beta} < 0)$: proportion of posterior samples that is smaller than 0 \rightarrow probability that parameter is smaller than 0 (i.e. speed-up)
- ► Go through script *BLMM_postprob*.*R*

- ▶ What's the most likely value for unknown parameter?
- ► Maximum A posteriori (MAP): most frequent ~ probable value
- ► Go through script *BLMM_MAP.R*

- ► Comparing hypotheses (i.e. models) using Bayes Factors (BF)
- ▶ BF_{10} : support for H_1 over H_0
- ▶ $BF_{10} = 2$: H_1 is two times more likely than H_0 ; convincing?
- ▶ $BF_{10} = 3-5$: weak to moderate evidence
- ▶ $BF_{10} > 10$: strong support
- ▶ BF_{10} < .3: evidence against H_1
- ▶ For evidence in favour of H_0 : BF_{01}
- Savage-Dickey density ratio (Dickey, Lientz, et al., 1970)
- ▶ see e.g. Baguley (2012), Dienes (2014), Lee and Wagenmakers (2014), Wagenmakers, Lodewyckx, Kuriyal, and Grasman (2010)
- ► Go through script *BLMM_BF.R*

- ► All you need!
- ► Model summary: *BLMM_modelsummary.R*



Posterior probability distribution of effect $\hat{\beta}$

Table: Estimates of BLMM. Evidence strongly supports H_1 ($BF_{10} > 5 \times 10^{34}$)

β	2.5%	97.5%	$P(\hat{\beta} < 0)$
51.12	47.98	54.26	< 0.001

- ► The future is Bayes!
- Existing probabilistic sampling software (Jags, Stan, WinBugs, pyMCMC) makes approximation of posterior easily possible.
- ▶ Open source access via *R* and *Python*.
- Complex models will converge (easy model fit).
- Answers the questions we ask
- …including support in favour of the null!
- ▶ No dichotomisation of the significance of the evidence.
- Probability distributions of possible parameter values.
- ► Interpretation of evidence is intuitive.
- Custom made models: mixture models, ex-Gaussian

- ▶ Introductions to using Bayesian linear mixed models:
 - ▶ Nicenboim and Vasishth (2016): applying *rstanarm* to psycholinguistic data
 - ▶ Sorensen, Hohenstein, and Vasishth (2016): building LMMs in Stan
- ► Bayesian theory:
 - ► Great books; with *R* code: Kruschke (2014), McElreath (2016)
 - Very technical; focus on hierarchical models: Gelman et al. (2014)

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